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SEQUENCE LISTING

<110> Adra, Chaker

<120> GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS AND USES THEREOF

<130> A0852.70000US01

<140> Not yet assigned

<141> 2006-09-05

<150> PCT/US2005/007519

<151> 2005-03-03

<150> 60/549,865

<151> 2004-03-03

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acgcccacct ccgcgcgcgc ccgcgcgcgt ctgcggccctc ccgcgtgcggc tctctggacg 180

ccatccccctc ctcacacctga agccaac atg aag gag acc cgg ggc tac gga ggg 234
Met Lys Glu Thr Arg Gly Tyr Gly Gly
1 5

gat gcc ccc ttc tgc acc cgc ctc aac cac tcc tac aca ggc atg tgg 282
Asp Ala Pro Phe Cys Thr Arg Leu Asn His Ser Tyr Thr Gly Met Trp
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gcg ccc gag cgt tcc gcc gag gcg cgg ggc aac ctc acg cgc cct cca 330
Ala Pro Glu Arg Ser Ala Glu Ala Arg Gly Asn Leu Thr Arg Pro Pro

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Gly Ser Gly Glu Asp Cys Gly Ser Val Ser Val Ala Phe Pro Ile Thr			
45	50	55	
atg ctg ctc act ggt ttc gtg ggc aac gca ctg gcc atg ctg ctc gtg			426
Met Leu Leu Thr Gly Phe Val Gly Asn Ala Leu Ala Met Leu Leu Val			
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tcg cgc agc tac cgg cgc cgg gag agc aag cgc aag aag tcc ttc ctg			474
Ser Arg Ser Tyr Arg Arg Glu Ser Lys Arg Lys Lys Ser Phe Leu			
75	80	85	
ctg tgc atc ggc tgg ctg gcg ctc acc gac ctg gtc ggg cag ctt ctc			522
Leu Cys Ile Gly Trp Leu Ala Leu Thr Asp Leu Val Gly Gln Leu Leu			
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acc acc ccg gtc gtc atc gtc gtg tac ctg tcc aag cag cgt tgg gag			570
Thr Thr Pro Val Val Ile Val Val Tyr Leu Ser Lys Gln Arg Trp Glu			
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His Ile Asp Pro Ser Gly Arg Leu Cys Thr Phe Phe Gly Leu Thr Met			
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act gtt ttc ggg ctc tcc tcg ttg ttc atc gcc agc gcc atg gcc gtc			666
Thr Val Phe Gly Leu Ser Ser Leu Phe Ile Ala Ser Ala Met Ala Val			
140	145	150	
gag cgg gcg ctg gcc atc agg gcg ccg cac tgg tat gcg agc cac atg			714
Glu Arg Ala Leu Ala Ile Arg Ala Pro His Trp Tyr Ala Ser His Met			
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Lys Thr Arg Ala Thr Arg Ala Val Leu Leu Gly Val Trp Leu Ala Val			
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ctc gcc ttc gcc ctg ctg ccg gtg ctg ggc gtg ggc cag tac acc gtc			810
Leu Ala Phe Ala Leu Leu Pro Val Leu Gly Val Gly Gln Tyr Thr Val			
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cag tgg ccc ggg acg tgg tgc ttc atc agc acc ggg cga ggg ggc aac			858
Gln Trp Pro Gly Thr Trp Cys Phe Ile Ser Thr Gly Arg Gly Gly Asn			
205	210	215	
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Gly Thr Ser Ser His Asn Trp Gly Asn Leu Phe Ala Ser Ala			
220	225	230	
ttt gcc ttc ctg ggg ctc ttg gcg ctg aca gtc acc ttt tcc tgc aac			954
Phe Ala Phe Leu Gly Leu Leu Ala Leu Thr Val Thr Phe Ser Cys Asn			
235	240	245	
ctg gcc acc att aag gcc ctg gtg tcc cgc tgc cgg gcc aag gcc acg			1002
Leu Ala Thr Ile Lys Ala Leu Val Ser Arg Cys Arg Ala Lys Ala Thr			
250	255	260	265
gca tct cag tcc agt gcc cag tgg ggc cgc atc acg acc gag acg gcc			1050
Ala Ser Gln Ser Ser Ala Gln Trp Gly Arg Ile Thr Thr Glu Thr Ala			
270	275	280	

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ctc ctg ata atg atg ttg aaa atg atc ttc aat cag aca tca gtt gag Leu Leu Ile Met Met Leu Lys Met Ile Phe Asn Gln Thr Ser Val Glu 300 305 310	1146
cac tgc aag aca cac acg gag aag cag aaa gaa tgc aac ttc ttc tta His Cys Lys Thr His Thr Glu Lys Gln Lys Glu Cys Asn Phe Phe Leu 315 320 325	1194
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tac ctg ctg tta aga aag atc ctt ctt cga aag ttt tgc cag atc agg Tyr Leu Leu Leu Arg Lys Ile Leu Leu Arg Lys Phe Cys Gln Ile Arg 350 355 360	1290
tac cac aca aac aac tat gca tcc agc tcc acc tcc tta ccc tgc cag Tyr His Thr Asn Asn Tyr Ala Ser Ser Ser Thr Ser Leu Pro Cys Gln 365 370 375	1338
tgt tcc tca acc ttg atg tgg agc gac cat ttg gaa aga taa Cys Ser Ser Thr Leu Met Trp Ser Asp His Leu Glu Arg 380 385 390	1380
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2344

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35 40 45

Ser Val Ser Val Ala Phe Pro Ile Thr Met Leu Leu Thr Gly Phe Val
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Gly Asn Ala Leu Ala Met Leu Leu Val Ser Arg Ser Tyr Arg Arg Arg
65 70 75 80

Glu Ser Lys Arg Lys Lys Ser Phe Leu Leu Cys Ile Gly Trp Leu Ala
85 90 95

Leu Thr Asp Leu Val Gly Gln Leu Leu Thr Thr Pro Val Val Ile Val
100 105 110

Val Tyr Leu Ser Lys Gln Arg Trp Glu His Ile Asp Pro Ser Gly Arg
115 120 125

Leu Cys Thr Phe Phe Gly Leu Thr Met Thr Val Phe Gly Leu Ser Ser
130 135 140

Leu Phe Ile Ala Ser Ala Met Ala Val Glu Arg Ala Leu Ala Ile Arg
145 150 155 160

Ala Pro His Trp Tyr Ala Ser His Met Lys Thr Arg Ala Thr Arg Ala
165 170 175

Val Leu Leu Gly Val Trp Leu Ala Val Leu Ala Phe Ala Leu Leu Pro
180 185 190

Val Leu Gly Val Gly Gln Tyr Thr Val Gln Trp Pro Gly Thr Trp Cys
195 200 205

Phe Ile Ser Thr Gly Arg Gly Gly Asn Gly Thr Ser Ser Ser His Asn
210 215 220

Trp Gly Asn Leu Phe Phe Ala Ser Ala Phe Ala Phe Leu Gly Leu Leu
225 230 235 240

Ala Leu Thr Val Thr Phe Ser Cys Asn Leu Ala Thr Ile Lys Ala Leu
245 250 255

Val Ser Arg Cys Arg Ala Lys Ala Thr Ala Ser Gln Ser Ser Ala Gln
260 265 270

Trp Gly Arg Ile Thr Thr Glu Thr Ala Ile Gln Leu Met Gly Ile Met
275 280 285

Cys Val Leu Ser Val Cys Trp Ser Pro Leu Leu Ile Met Met Leu Lys
290 295 300

Met Ile Phe Asn Gln Thr Ser Val Glu His Cys Lys Thr His Thr Glu
305 310 315 320

Lys Gln Lys Glu Cys Asn Phe Phe Leu Ile Ala Val Arg Leu Ala Ser
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340 345 350

Leu Leu Arg Lys Phe Cys Gln Ile Arg Tyr His Thr Asn Asn Tyr Ala
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Leu Leu Phe Trp Gly Cys Cys Val Met His Ser Trp Glu Gly His Ile							
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Arg Pro Thr Arg Lys Pro Asn Thr Lys Gly Asn Asn Cys Arg Asp Ser							
25 30 35							
acc ttg tgc cca gct tat gcc acc tgc acc aat aca gtc gac agt tac							200
Thr Leu Cys Pro Ala Tyr Ala Thr Cys Thr Asn Thr Val Asp Ser Tyr							
40 45 50							
tat tgc gct tgc aaa caa ggc ttc ctg tcc agc aat ggg caa aat cac							248
Tyr Cys Ala Cys Lys Gln Gly Phe Leu Ser Ser Asn Gly Gln Asn His							
55 60 65 70							
ttc aag gat cca gga gtc cga tgc aaa gat att gat gaa tgt tct caa							296
Phe Lys Asp Pro Gly Val Arg Cys Lys Asp Ile Asp Glu Cys Ser Gln							
75 80 85							
agc ccc cag ccc tgt ggt cct aac tca tcc tgc aaa aac ctg tca ggg							344
Ser Pro Gln Pro Cys Gly Pro Asn Ser Ser Cys Lys Asn Leu Ser Gly							
90 95 100							
agg tac aag tgc agc tgt tta gat ggt ttc tct tct ccc act gga aat							392
Arg Tyr Lys Cys Ser Cys Leu Asp Gly Ser Ser Pro Thr Gly Asn							
105 110 115							
gac tgg gtc cca gga aag ccg ggc aat ttc tcc tgt act gat atc aat							440
Asp Trp Val Pro Gly Lys Pro Gly Asn Phe Ser Cys Thr Asp Ile Asn							
120 125 130							
gag tgc ctc acc agc agc gtc tgc cct gag cat tct gac tgt gtc aac							488
Glu Cys Leu Thr Ser Ser Val Cys Pro Glu His Ser Asp Cys Val Asn							
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Ser Met Gly Ser Tyr Ser Cys Ser Cys Gln Val Gly Phe Ile Ser Arg							
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Asn Ser Thr Cys Glu Asp Val Asp Glu Cys Ala Asp Pro Arg Ala Cys							
170 175 180							
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Pro Glu His Ala Thr Cys Asn Thr Val Gly Asn Tyr Ser Cys Phe							
185 190 195							
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Cys Asn Pro Gly Phe Glu Ser Ser Gly His Leu Ser Phe Gln Gly							
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Leu Lys Ala Ser Cys Glu Asp Ile Asp Glu Cys Thr Glu Met Cys Pro							
215 220 225 230							
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Ile Asn Ser Thr Cys Thr Asn Thr Pro Gly Ser Tyr Phe Cys Thr Cys							

235	240	245	
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gga gtg gaa tgt aga gat att gat gag tgc cgc caa gat cca tca acc Gly Val Glu Cys Arg Asp Ile Asp Glu Cys Arg Gln Asp Pro Ser Thr 265 270 275			872
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gcc aag ggg gat aag atg aag atc ggg tgt tcc aca att gag gaa tct Ala Lys Gly Asp Lys Met Lys Ile Gly Cys Ser Thr Ile Glu Glu Ser 455 460 465 470			1448
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act ctg gag aac att cag cca aag cag aag ttt gag agg ccc atc tgt Thr Leu Glu Asn Ile Gln Pro Lys Gln Lys Phe Glu Arg Pro Ile Cys 535 540 545 550	1688
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cag atg gca aat ctt gcc gtt atc atg gcg tct ggg gag ctc acg atg Gln Met Ala Asn Leu Ala Val Ile Met Ala Ser Gly Glu Leu Thr Met 585 590 595	1832
gac ttt tcc ttg tac atc att agc cat gta ggc att atc atc tcc ttg Asp Phe Ser Leu Tyr Ile Ile Ser His Val Gly Ile Ile Ile Ser Leu 600 605 610	1880
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Asn Thr Val Asp Ser Tyr Tyr Cys Ala Cys Lys Gln Gly Phe Leu Ser
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Ser Asn Gly Gln Asn His Phe Lys Asp Pro Gly Val Arg Cys Lys Asp
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Ile Asp Glu Cys Ser Gln Ser Pro Gln Pro Cys Gly Pro Asn Ser Ser
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Cys Lys Asn Leu Ser Gly Arg Tyr Lys Cys Ser Cys Leu Asp Gly Phe
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Ser Ser Pro Thr Gly Asn Asp Trp Val Pro Gly Lys Pro Gly Asn Phe
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Ser Cys Thr Asp Ile Asn Glu Cys Leu Thr Ser Ser Val Cys Pro Glu
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His Ser Asp Cys Val Asn Ser Met Gly Ser Tyr Ser Cys Ser Cys Gln
145 150 155 160

Val Gly Phe Ile Ser Arg Asn Ser Thr Cys Glu Asp Val Asp Glu Cys
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Ala Asp Pro Arg Ala Cys Pro Glu His Ala Thr Cys Asn Asn Thr Val
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Gly Asn Tyr Ser Cys Phe Cys Asn Pro Gly Phe Glu Ser Ser Ser Gly
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Cys Thr Glu Met Cys Pro Ile Asn Ser Thr Cys Thr Asn Thr Pro Gly
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Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Pro Ser Asn Gly Gln
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Leu Asn Phe Thr Asp Gln Gly Val Glu Cys Arg Asp Ile Asp Glu Cys
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Arg Gln Asp Pro Ser Thr Cys Gly Pro Asn Ser Ile Cys Thr Asn Ala
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Gln Glu Gly Thr Ala Val Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln
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Gly Ile Ile Ile Ser Leu Val Cys Leu Val Leu Ala Ile Ala Thr Phe
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645 650 655

His Lys Thr Asp Asn Lys Met Gly Cys Ala Ile Ile Ala Gly Phe Leu
660 665 670

His Tyr Leu Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val
675 680 685

Ile Leu Phe Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser
690 695 700

Ser Arg Asn Ile Lys Met Leu His Ile Cys Ala Phe Gly Tyr Gly Leu
705 710 715 720

Pro Met Leu Val Val Val Ile Ser Ala Ser Val Gln Pro Gln Gly Tyr
725 730 735

Gly Met His Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp
740 745 750

Ser Phe Leu Gly Pro Val Cys Thr Val Ile Val Ile Asn Ser Leu Leu
755 760 765

Leu Thr Trp Thr Leu Trp Ile Leu Arg Gln Arg Leu Ser Ser Val Asn
770 775 780

Ala Glu Val Ser Thr Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala
785 790 795 800

Phe Ala Gln Leu Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe
805 810 815

Gln Ile Gly Pro Val Ala Gly Val Met Ala Tyr Leu Phe Thr Ile Ile
820 825 830

Asn Ser Leu Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn
835 840 845

Gly Gln Val Arg Glu Glu Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys
850 855 860

Pro Ser Ser Gln Ser Gln Thr Ser Arg Ile Leu Leu Ser Ser Met Pro
865 870 875 880

Ser Ala Ser Lys Thr Gly
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<211> 2428

<212> DNA

<213> Homo sapiens

<220>

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<222> (213)..(1229)

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aaacgctcac tggcaaaac accttcactg aaaagagacc tcatattatg caaaaaaaaaat 180

ctaaaaaggc ctctgccttc agaagttaca ag atg atc aat tca acc tcc aca Gln Pro Pro Asp Glu Ser Cys Ser Gln Asn Leu Leu Ile Thr Gln Gln	1	5	233
cag cct cca gat gaa tcc tgc tct cag aac ctc ctg atc act act cag cag 10 15 20			281
atc att cct gtg ctg tac tgt atg gtc ttc att gca gga atc cta ctc Ile Ile Pro Val Leu Tyr Cys Met Val Phe Ile Ala Gly Ile Leu Leu 25 30 35			329
aat gga gtg tca gga tgg ata ttc ttt tac gtg ccc agc tct gag agt Asn Gly Val Ser Gly Trp Ile Phe Phe Tyr Val Pro Ser Ser Glu Ser 40 45 50 55			377
ttc atc atc tat ctc aag aac att gtt att gct gac ttt gtg atg agc Phe Ile Ile Tyr Leu Lys Asn Ile Val Ile Ala Asp Phe Val Met Ser 60 65 70			425
ctg act ttt cct ttc aag atc ctt ggt gac tca ggc ctt ggt ccc tgg Leu Thr Phe Pro Phe Lys Ile Leu Gly Asp Ser Gly Leu Gly Pro Trp 75 80 85			473
cag ctg aac gtg ttt gtg tgc agg gtc tct gcc gtg ctc ttc tac gtc Gln Leu Asn Val Phe Val Cys Arg Val Ser Ala Val Leu Phe Tyr Val 90 95 100			521
aac atg tac gtc agc att gtg ttc ttt ggg ctc atc agc ttt gac aga Asn Met Tyr Val Ser Ile Val Phe Phe Gly Leu Ile Ser Phe Asp Arg 105 110 115			569
tat tat aaa att gta aag cct ctt tgg act tct ttc atc cag tca gtg Tyr Tyr Lys Ile Val Lys Pro Leu Trp Thr Ser Phe Ile Gln Ser Val 120 125 130 135			617
agt tac agc aaa ctt ctg tca gtg ata gta tgg atg ctc atg ctc ctc Ser Tyr Ser Lys Leu Leu Ser Val Ile Val Trp Met Leu Met Leu Leu 140 145 150			665
ctt gct gtt cca aat att att ctc acc aac cag agt gtt agg gag gtt Leu Ala Val Pro Asn Ile Ile Leu Thr Asn Gln Ser Val Arg Glu Val 155 160 165			713
aca caa ata aaa tgt ata gaa ctg aaa agt gaa ctg gga cgg aag tgg Thr Gln Ile Lys Cys Ile Glu Leu Lys Ser Glu Leu Gly Arg Lys Trp 170 175 180			761
cac aaa gca tca aac tac atc ttc gtg gcc atc ttc tgg att gtg ttt His Lys Ala Ser Asn Tyr Ile Phe Val Ala Ile Phe Trp Ile Val Phe 185 190 195			809
ctt ttg tta atc gtt ttc tat act gct atc aca aag aaa atc ttt aag Leu Leu Leu Ile Val Phe Tyr Thr Ala Ile Thr Lys Lys Ile Phe Lys 200 205 210 215			857
tcc cac ctt aag tca agt cgg aat tcc act tcg gtc aaa aag aaa tct Ser His Leu Lys Ser Ser Arg Asn Ser Thr Ser Val Lys Lys Lys Ser 220 225 230			905
agc cgc aac ata ttc agc atc gtg ttt gtg ttt ttt gtc tgg ttt gta			953

Ser Arg Asn Ile Phe Ser Ile Val Phe Val Phe Phe Val Cys Phe Val			
235	240	245	
cct tac cat att gcc aga atc ccc tac aca aag agt cag acc gaa gct			1001
Pro Tyr His Ile Ala Arg Ile Pro Tyr Thr Lys Ser Gln Thr Glu Ala			
250	255	260	
cat tac agc tgc cag tca aaa gaa atc ttg cggtat atg aaa gaa ttc			1049
His Tyr Ser Cys Gln Ser Lys Glu Ile Leu Arg Tyr Met Lys Glu Phe			
265	270	275	
act ctg cta cta tct gct gca aat gta tgc ttg gac cct att att tat			1097
Thr Leu Leu Leu Ser Ala Ala Asn Val Cys Leu Asp Pro Ile Ile Tyr			
280	285	290	295
ttc ttt cta tgc cag ccgtttt agg gaa atc tta tgt aag aaa ttg cac			1145
Phe Phe Leu Cys Gln Pro Phe Arg Glu Ile Leu Cys Lys Lys Leu His			
300	305	310	
att cca tta aaa gct cag aat gac cta gac att tcc aga atc aaa aga			1193
Ile Pro Leu Lys Ala Gln Asn Asp Leu Asp Ile Ser Arg Ile Lys Arg			
315	320	325	
gga aat aca aca ctt gaa agc aca gat act ttg tga gttcctaccc			1239
Gly Asn Thr Thr Leu Glu Ser Thr Asp Thr Leu			
330	335		
tcttccaaag aaagaccacg tgcgtatgtt gtcatcttca attacataac agaaatcaat			1299
aagatatgtg ccctcatcat aaatatcatc tcttagcactg ccatccaatt tagttcaata			1359
aaattcaaat ataagtttcc atgctttttt gtaacatcaa agaaaacata cccatcagta			1419
atttctctaa tactgacctt tctattctct attaataaaa aattaataca tacaattatt			1479
caattctatt atattaaaat aagtaaaat ttataaccac tagtctggc agttaatgta			1539
gaaatttaaa tagtaaataa aacacaacat aatcaaagac aactcactca ggcattttct			1599
ttctctaaat accagaatct agtatgtaat tgtttcaac actgtcctta aagactaact			1659
tgaaagcagg cacagttga tgaaggcgtt gagagctgtt tgcaataaaa agtcagggtt			1719
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caaagactta cgtcattaa tgagcctggg gttctgggt tagaatattt ttaagtaggc			1959
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agctacccaaa actaaattct ttctctgcta ttaactggct agaagacatt catctatttt 2319
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<210> 11
<211> 338
<212> PRT
<213> Homo sapiens

<400> 11

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20 25 30

Phe Ile Ala Gly Ile Leu Leu Asn Gly Val Ser Gly Trp Ile Phe Phe
35 40 45

Tyr Val Pro Ser Ser Glu Ser Phe Ile Ile Tyr Leu Lys Asn Ile Val
50 55 60

Ile Ala Asp Phe Val Met Ser Leu Thr Phe Pro Phe Lys Ile Leu Gly
65 70 75 80

Asp Ser Gly Leu Gly Pro Trp Gln Leu Asn Val Phe Val Cys Arg Val
85 90 95

Ser Ala Val Leu Phe Tyr Val Asn Met Tyr Val Ser Ile Val Phe Phe
100 105 110

Gly Leu Ile Ser Phe Asp Arg Tyr Tyr Lys Ile Val Lys Pro Leu Trp
115 120 125

Thr Ser Phe Ile Gln Ser Val Ser Tyr Ser Lys Leu Leu Ser Val Ile
130 135 140

Val Trp Met Leu Met Leu Leu Ala Val Pro Asn Ile Ile Leu Thr
145 150 155 160

Asn Gln Ser Val Arg Glu Val Thr Gln Ile Lys Cys Ile Glu Leu Lys
165 170 175

Ser Glu Leu Gly Arg Lys Trp His Lys Ala Ser Asn Tyr Ile Phe Val
180 185 190

Ala Ile Phe Trp Ile Val Phe Leu Leu Leu Ile Val Phe Tyr Thr Ala
195 200 205

Ile Thr Lys Lys Ile Phe Lys Ser His Leu Lys Ser Ser Arg Asn Ser
210 215 220

Thr Ser Val Lys Lys Ser Ser Arg Asn Ile Phe Ser Ile Val Phe
225 230 235 240

Val Phe Phe Val Cys Phe Val Pro Tyr His Ile Ala Arg Ile Pro Tyr
245 250 255

Thr Lys Ser Gln Thr Glu Ala His Tyr Ser Cys Gln Ser Lys Glu Ile
260 265 270

Leu Arg Tyr Met Lys Glu Phe Thr Leu Leu Leu Ser Ala Ala Asn Val
275 280 285

Cys Leu Asp Pro Ile Ile Tyr Phe Phe Leu Cys Gln Pro Phe Arg Glu
290 295 300

Ile Leu Cys Lys Lys Leu His Ile Pro Leu Lys Ala Gln Asn Asp Leu
305 310 315 320

Asp Ile Ser Arg Ile Lys Arg Gly Asn Thr Thr Leu Glu Ser Thr Asp
325 330 335

Thr Leu

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Met Val Ile Met Gly Gln Cys Tyr Tyr
1 5

aac gag acc atc ggc ttc ttc tat aac aac agt ggc aaa gag ctc agc 159
Asn Glu Thr Ile Gly Phe Phe Tyr Asn Asn Ser Gly Lys Glu Leu Ser
10 15 20 25

tcc cac tgg cgg ccc aag gat gtg gtc gtg gca ctg ggg ctg acc	207
Ser His Trp Arg Pro Lys Asp Val Val Val Ala Leu Gly Leu Thr	
30 35 40	
gtc agc gtg ctg gtg ctg acc aat ctg ctg gtc ata gca gcc atc	255
Val Ser Val Leu Val Leu Leu Thr Asn Leu Leu Val Ile Ala Ala Ile	
45 50 55	
gcc tcc aac cgc cgc ttc cac cag ccc atc tac tac ctg ctc ggc aat	303
Ala Ser Asn Arg Arg Phe His Gln Pro Ile Tyr Tyr Leu Leu Gly Asn	
60 65 70	
ctg gcc gcg gct gac ctc ttc gcg ggc gtg gcc tac ctc ttc ctc atg	351
Leu Ala Ala Ala Asp Leu Phe Ala Gly Val Ala Tyr Leu Phe Leu Met	
75 80 85	
ttc cac act ggt ccc cgc aca gcc cga ctt tca ctt gag ggc tgg ttc	399
Phe His Thr Gly Pro Arg Thr Ala Arg Leu Ser Leu Glu Gly Trp Phe	
90 95 100 105	
ctg cgg cag ggc ttg ctg gac aca agc ctc act gcg tcg gtg gcc aca	447
Leu Arg Gln Gly Leu Leu Asp Thr Ser Leu Thr Ala Ser Val Ala Thr	
110 115 120	
ctg ctg gcc atc gcc gtg gag cgg cac cgc agt gtg atg gcc gtg cag	495
Leu Leu Ala Ile Ala Val Glu Arg His Arg Ser Val Met Ala Val Gln	
125 130 135	
ctg cac agc cgc ctg ccc cgt ggc cgc gtg gtc atg ctc att gtg ggc	543
Leu His Ser Arg Leu Pro Arg Gly Arg Val Val Met Leu Ile Val Gly	
140 145 150	
gtg tgg gtg gct gcc ctg ggc ctg ggg ctg ctg cct gcc cac tcc tgg	591
Val Trp Val Ala Ala Leu Gly Leu Gly Leu Leu Pro Ala His Ser Trp	
155 160 165	
cac tgc ctc tgt gcc ctg gac cgc tgc tca cgc atg gca ccc ctg ctc	639
His Cys Leu Cys Ala Leu Asp Arg Cys Ser Arg Met Ala Pro Leu Leu	
170 175 180 185	
agc cgc tcc tat ttg gcc gtc tgg gct ctg tcg agc ctg ctt gtc ttc	687
Ser Arg Ser Tyr Leu Ala Val Trp Ala Leu Ser Ser Leu Leu Val Phe	
190 195 200	
ctg ctc atg gtg gct gtg tac acc cgc att ttc ttc tac gtg cgg cgg	735
Leu Leu Met Val Ala Val Tyr Thr Arg Ile Phe Phe Tyr Val Arg Arg	
205 210 215	
cga gtg cag cgc atg gca gag cat gtc agc tgc cac ccc cgc tac cga	783
Arg Val Gln Arg Met Ala Glu His Val Ser Cys His Pro Arg Tyr Arg	
220 225 230	
gag acc acg ctc agc ctg gtc aag act gtt gtc atc atc ctg ggg gcg	831
Glu Thr Thr Leu Ser Leu Val Lys Thr Val Val Ile Ile Leu Gly Ala	
235 240 245	
ttc gtg gtc tgc tgg aca cca ggc cag gtg gta ctg ctc ctg gat ggt	879
Phe Val Val Cys Trp Thr Pro Gly Gln Val Val Leu Leu Leu Asp Gly	
250 255 260 265	

tta ggc tgt gag tcc tgc aat gtc ctg gct gta gaa aag tac ttc cta	927		
Leu Gly Cys Glu Ser Cys Asn Val Leu Ala Val Glu Lys Tyr Phe Leu			
270	275	280	
ctg ttg gcc gag gcc aac tca ctg gtc aat gct gct gtg tac tct tgc	975		
Leu Leu Ala Glu Ala Asn Ser Leu Val Asn Ala Ala Val Tyr Ser Cys			
285	290	295	
cga gat gct gag atg cgc cgc acc ttc cgc cgc ctt ctc tgc tgc gcg	1023		
Arg Asp Ala Glu Met Arg Arg Thr Phe Arg Arg Leu Leu Cys Cys Ala			
300	305	310	
tgc ctc cgc cag tcc acc cgc gag tct gtc cac tat aca tcc tct gcc	1071		
Cys Leu Arg Gln Ser Thr Arg Glu Ser Val His Tyr Thr Ser Ser Ala			
315	320	325	
cag gga ggt gcc agc act cgc atc atg ctt ccc gag aac ggc cac cca	1119		
Gln Gly Gly Ala Ser Thr Arg Ile Met Leu Pro Glu Asn Gly His Pro			
330	335	340	345
ctg atg act cca ccc ttt agc tac ctt gaa ctt cag cgg tac gcg gca	1167		
Leu Met Thr Pro Pro Phe Ser Tyr Leu Glu Leu Gln Arg Tyr Ala Ala			
350	355	360	
agc aac aaa tcc aca gcc cct gat gac ttg tgg gtg ctc ctg gct caa	1215		
Ser Asn Lys Ser Thr Ala Pro Asp Asp Leu Trp Val Leu Leu Ala Gln			
365	370	375	
ccc aac caa cag gac tga ctgactggca ggacaaggc tggcatggca	1263		
Pro Asn Gln Gln Asp			
380			
cagcaccact gccaggcctc cccaggcaca ccactctgcc caggaatgg gggctttggg	1323		
tcatctccca ctgcctgggg gagtcagatg gggcagga atctggctct tcagccatct	1383		
caggtttagg gggttttaa cagacattat tctgtttca ctgcgtatcc ttggtaagcc	1443		
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ctctcgggcc atgctacccg gtatgactgg gtaatgagga cagactgtgg acacccatc	1563		
tacctgagtc tgattctta gcagcagaga ctgaggggtg cagagtgtga gctggaaag	1623		
gtttgtggct cttgcagcc tccagggact ggcctgtccc caatagaatt gaagcagtcc	1683		
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Tyr Asn Asn Ser Gly Lys Glu Leu Ser Ser His Trp Arg Pro Lys Asp			

20

25

30

Val Val Val Val Ala Leu Gly Leu Thr Val Ser Val Leu Val Leu Leu
35 40 45

Thr Asn Leu Leu Val Ile Ala Ala Ile Ala Ser Asn Arg Arg Phe His
50 55 60

Gln Pro Ile Tyr Tyr Leu Leu Gly Asn Leu Ala Ala Ala Asp Leu Phe
65 70 75 80

Ala Gly Val Ala Tyr Leu Phe Leu Met Phe His Thr Gly Pro Arg Thr
85 90 95

Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu Leu Asp
100 105 110

Thr Ser Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala Val Glu
115 120 125

Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu Pro Arg
130 135 140

Gly Arg Val Val Met Leu Ile Val Gly Val Trp Val Ala Ala Leu Gly
145 150 155 160

Leu Gly Leu Leu Pro Ala His Ser Trp His Cys Leu Cys Ala Leu Asp
165 170 175

Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val
180 185 190

Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr
195 200 205

Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu
210 215 220

His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val
225 230 235 240

Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro
245 250 255

Gly Gln Val Val Leu Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn
260 265 270

Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser
275 280 285

Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ala Glu Met Arg Arg
290 295 300

Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg
305 310 315 320

Glu Ser Val His Tyr Thr Ser Ser Ala Gln Gly Gly Ala Ser Thr Arg
325 330 335

Ile Met Leu Pro Glu Asn Gly His Pro Leu Met Thr Pro Pro Phe Ser
340 345 350

Tyr Leu Glu Leu Gln Arg Tyr Ala Ala Ser Asn Lys Ser Thr Ala Pro
355 360 365

Asp Asp Leu Trp Val Leu Leu Ala Gln Pro Asn Gln Gln Asp
370 375 380

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<211> 993
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(993)

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Met Leu Pro Asp Trp Lys Ser Ser Leu Ile Leu Met Ala Tyr Ile Ile
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atc ttc ctc act ggc ctc cct gcc aac ctc ctg gcc ctg cggtt
Ile Phe Leu Thr Gly Leu Pro Ala Asn Leu Leu Ala Leu Arg Ala Phe
20 25 30 96

gtg ggg cgg atc cgc cag ccc cag cct gca cct gtg cac atc ctc ctg
Val Gly Arg Ile Arg Gln Pro Gln Pro Ala Pro Val His Ile Leu Leu
35 40 45 144

ctg agc ctg acg ctg gcc gac ctc ctc ctg ctg ctg ctg ccc ttc
Leu Ser Leu Thr Leu Ala Asp Leu Leu Leu Leu Leu Leu Pro Phe
50 55 60 192

aag atc atc gag gct gcg aac ttc cgc tgg tac ctg ccc aag gtc
Lys Ile Ile Glu Ala Ala Ser Asn Phe Arg Trp Tyr Leu Pro Lys Val
65 70 75 80 240

gtc tgc gcc ctc acg agt ttt ggc ttc tac agc agc atc tac tgc agc Val Cys Ala Leu Thr Ser Phe Gly Phe Tyr Ser Ser Ile Tyr Cys Ser 85	90	95	288
acg tgg ctc ctg gcg ggc atc agc atc gag cgc tac ctg gga gtg gct Thr Trp Leu Leu Ala Gly Ile Ser Ile Glu Arg Tyr Leu Gly Val Ala 100	105	110	336
ttc ccc gtg cag tac aag ctc tcc cgc cgg cct ctg tat gga gtg att Phe Pro Val Gln Tyr Lys Leu Ser Arg Arg Pro Leu Tyr Gly Val Ile 115	120	125	384
gca gct ctg gtg gcc tgg gtt atg tcc ttt ggt cac tgc acc atc gtg Ala Ala Leu Val Ala Trp Val Met Ser Phe Gly His Cys Thr Ile Val 130	135	140	432
atc atc gtt caa tac ttg aac acg act gag cag gtc aga agt ggc aat Ile Ile Val Gln Tyr Leu Asn Thr Glu Gln Val Arg Ser Gly Asn 145	150	155	480
gaa att acc tgc tac gag aac ttc acc gat aac cag ttg gac gtg gtg Glu Ile Thr Cys Tyr Glu Asn Phe Thr Asp Asn Gln Leu Asp Val Val 165	170	175	528
ctg ccc gtg cgg ctg gag ctg tgc ctg gtg ctc ttc atc ccc atg Leu Pro Val Arg Leu Glu Leu Cys Leu Val Leu Phe Phe Ile Pro Met 180	185	190	576
gca gtc acc atc ttc tgc tac tgg cgt ttt gtg tgg atc atg ctc tcc Ala Val Thr Ile Phe Cys Tyr Trp Arg Phe Val Trp Ile Met Leu Ser 195	200	205	624
cag ccc ctt gtg ggg gcc cag agg cgg cgc cga gcc gtg ggg ctg gct Gln Pro Leu Val Gly Ala Gln Arg Arg Arg Ala Val Gly Leu Ala 210	215	220	672
gtg gtg acg ctg ctc aat ttc ctg gtg tgc ttc gga cct tac aac gtg Val Val Thr Leu Leu Asn Phe Leu Val Cys Phe Gly Pro Tyr Asn Val 225	230	235	720
tcc cac ctg gtg ggg tat cac cag aga aaa agc ccc tgg tgg cgg tca Ser His Leu Val Gly Tyr His Gln Arg Lys Ser Pro Trp Trp Arg Ser 245	250	255	768
ata gcc gtg ttc agt tca ctc aac gcc agt ctg gac ccc ctg ctc Ile Ala Val Val Phe Ser Ser Leu Asn Ala Ser Leu Asp Pro Leu Leu 260	265	270	816
ttc tat ttc tct tca gtg gtg cgc agg gca ttt ggg aga ggg ctg Phe Tyr Phe Ser Ser Val Val Arg Arg Ala Phe Gly Arg Gly Leu 275	280	285	864
cag gtg ctg cgg aat cag ggc tcc tcc ctg ttg gga cgc aga ggc aaa Gln Val Leu Arg Asn Gln Gly Ser Ser Leu Leu Gly Arg Arg Gly Lys 290	295	300	912
gac aca gca gag ggg aca aat gag gac agg ggt gtg ggt caa gga gaa Asp Thr Ala Glu Gly Thr Asn Glu Asp Arg Gly Val Gly Gln Gly Glu 305	310	315	960
ggg atg cca agt tcg gac ttc act aca gag tag			993

Gly Met Pro Ser Ser Asp Phe Thr Thr Glu
325 330

<210> 15
<211> 330
<212> PRT
<213> Homo sapiens

<400> 15

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Ile Phe Leu Thr Gly Leu Pro Ala Asn Leu Leu Ala Leu Arg Ala Phe
20 , 25 30

Val Gly Arg Ile Arg Gln Pro Gln Pro Ala Pro Val His Ile Leu Leu
35 40 45

Leu Ser Leu Thr Leu Ala Asp Leu Leu Leu Leu Leu Pro Phe
50 55 60

Lys Ile Ile Glu Ala Ala Ser Asn Phe Arg Trp Tyr Leu Pro Lys Val
65 70 75 80

Val Cys Ala Leu Thr Ser Phe Gly Phe Tyr Ser Ser Ile Tyr Cys Ser
85 90 95

Thr Trp Leu Leu Ala Gly Ile Ser Ile Glu Arg Tyr Leu Gly Val Ala
100 105 110

Phe Pro Val Gln Tyr Lys Leu Ser Arg Arg Pro Leu Tyr Gly Val Ile
115 120 125

Ala Ala Leu Val Ala Trp Val Met Ser Phe Gly His Cys Thr Ile Val
130 135 140 145

Ile Ile Val Gln Tyr Leu Asn Thr Thr Glu Gln Val Arg Ser Gly Asn
145 150 155 160

Glu Ile Thr Cys Tyr Glu Asn Phe Thr Asp Asn Gln Leu Asp Val Val
165 170 175

Leu Pro Val Arg Leu Glu Leu Cys Leu Val Leu Phe Phe Ile Pro Met
180 185 190

Ala Val Thr Ile Phe Cys Tyr Trp Arg Phe Val Trp Ile Met Leu Ser
195 200 205

Gln Pro Leu Val Gly Ala Gln Arg Arg Arg Arg Ala Val Gly Leu Ala
210 215 220

Val Val Thr Leu Leu Asn Phe Leu Val Cys Phe Gly Pro Tyr Asn Val
225 230 235 240

Ser His Leu Val Gly Tyr His Gln Arg Lys Ser Pro Trp Trp Arg Ser
245 250 255

Ile Ala Val Val Phe Ser Ser Leu Asn Ala Ser Leu Asp Pro Leu Leu
260 265 270

Phe Tyr Phe Ser Ser Ser Val Val Arg Arg Ala Phe Gly Arg Gly Leu
275 280 285

Gln Val Leu Arg Asn Gln Gly Ser Ser Leu Leu Gly Arg Arg Gly Lys
290 295 300

Asp Thr Ala Glu Gly Thr Asn Glu Asp Arg Gly Val Gly Gln Gly Glu
305 310 315 320

Gly Met Pro Ser Ser Asp Phe Thr Thr Glu
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<212> DNA

<213> Homo sapiens

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<222> (72)..(1085)

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Met Gly Asn Asp Ser Val Ser Tyr Glu Tyr Gly Asp Tyr
1 5 10

agc gac ctc tcg gac cgc cct gtg gac tgc ctg gat ggc gcc tgc ctg 158
Ser Asp Leu Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu
15 20 25

gcc atc gac ccg ctg cgc gtg gcc ccg ctc cca ctg tat gcc gcc atc 206
Ala Ile Asp Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile
30 35 40 45

ttc ctg gtg ggg gtg ccg ggc aat gcc atg gtg gcc tgg gtg gct ggg 254
Phe Leu Val Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly

50	55	60	
aag gtg gcc cgc cgg agg gtg ggt gcc acc tgg ttg ctc cac ctg gcc Lys Val Ala Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala 65 70 75			302
gtg gcg gat ttg ctg tgc tgt ttg tct ctg ccc atc ctg gca gtg ccc Val Ala Asp Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro 80 85 90			350
att gcc cgt gga ggc cac tgg ccg tat ggt gca gtg ggc tgt cgg gcg Ile Ala Arg Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala 95 100 105			398
ctg ccc tcc atc atc ctg ctg acc atg tat gcc agc gtc ctg ctc ctg Leu Pro Ser Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Leu 110 115 120 125			446
gca gct ctc agt gcc gac ctc tgc ttc ctg gct ctc ggg cct gcc tgg Ala Ala Leu Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp 130 135 140			494
tgg tct acg gtt cag cgg gcg tgc ggg gtg cag gtg gcc tgt ggg gca Trp Ser Thr Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala 145 150 155			542
gcc tgg aca ctg gcc ttg ctg ctc acc gtg ccc tcc gcc atc tac cgc Ala Trp Thr Leu Ala Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg 160 165 170			590
cgg ctg cac cag gag cac ttc cca gcc cgg ctg cag tgt gtg gtg gac Arg Leu His Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp 175 180 185			638
tac ggc ggc tcc tcc agc acc gag aat gcg gtg act gcc atc cgg ttt Tyr Gly Gly Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe 190 195 200 205			686
ctt ttt ggc ttc ctg ggg ccc ctg gtg gcc gtg gcc agc tgc cac agt Leu Phe Gly Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser 210 215 220			734
gcc ctc ctg tgc tgg gca gcc cga cgc tgc cgg ccg ctg ggc aca gcc Ala Leu Leu Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala 225 230 235			782
att gtg gtg ggg ttt ttt gtc tgc tgg gca ccc tac cac ctg ctg ggg Ile Val Val Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Leu Gly 240 245 250			830
ctg gtg ctc act gtg gcg gcc ccg aac tcc gca ctc ctg gcc agg gcc Leu Val Leu Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala 255 260 265			878
ctg cgg gct gaa ccc ctc atc gtg ggc ctt gcc ctc gct cac agc tgc Leu Arg Ala Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys 270 275 280 285			926
ctc aat ccc atg ctc ttc ctg tat ttt ggg agg gct caa ctc cgc cgg Leu Asn Pro Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg 290 295 300			974

tca ctg cca gct gcc tgt cac tgg gcc ctg agg gag tcc cag ggc cag 1022
Ser Leu Pro Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln
305 310 315

gac gaa agt gtg gac agc aag aaa tcc acc agc cat gac ctg gtc tcg 1070
Asp Glu Ser Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser
320 325 330

gag atg gag gtg tag gctggagaga cattgtgggt gtgtatcttc ttatctcatt 1125
Glu Met Glu Val
335

tcacaagact ggcttcaggc atagctggat ccaggagctc aatgatgtct tcattttatt 1185
ccttccttca ttcaacagat atccatcatg cacttgctat gtgcaaggcc tttttaggca 1245
ctagagatat agcagtgacc aaaacagaca caaatcctgc cc 1287

<210> 17
<211> 337
<212> PRT
<213> Homo sapiens

<400> 17

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1 5 10 15

Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp
20 25 30

Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile Phe Leu Val
35 40 45

Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala
50 55 60

Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala Val Ala Asp
65 70 75 80

Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro Ile Ala Arg
85 90 95

Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala Leu Pro Ser
100 105 110

Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Ala Ala Leu
115 120 125

Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp Trp Ser Thr
130 135 140

Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala Ala Trp Thr
145 150 155 160

Leu Ala Leu Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg Arg Leu His
165 170 175

Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp Tyr Gly Gly
180 185 190

Ser Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe Leu Phe Gly
195 200 205

Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser Ala Leu Leu
210 215 220

Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala Ile Val Val
225 230 235 240

Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Leu Gly Leu Val Leu
245 250 255

Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala Leu Arg Ala
260 265 270

Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys Leu Asn Pro
275 280 285

Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg Ser Leu Pro
290 295 300

Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln Asp Glu Ser
305 310 315 320

Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser Glu Met Glu
325 330 335

Val

<210> 18
<211> 2858
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (174)..(1175)

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atgctataaa cataaaagtct gttttaaaa aatagcattt gaaaatcatg aagggtttt 120
tgttttcttt tgtttgata tatgtttatt ggtaacaggt gacactggaa gca atg 176
Met
1

aac acc aca gtg atg caa ggc ttc aac aga tct gag cgg tgc ccc aga 224
Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro Arg
5 10 15

gac act cggttata gta cag ctg gta ttc cca gcc ctc tac aca gtg gtt 272
Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val Val
20 25 30

ttc ttg acc ggc atc ctg ctg aat act ttg gct ctg tgg gtg ttt gtt 320
Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe Val
35 40 45

cac atc ccc agc tcc tcc acc ttc atc atc tac ctc aaa aac act ttg 368
His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr Leu
50 55 60 65

gtg gcc gac ttg ata atg aca ctc atg ctt cct ttc aaa atc ctc tct 416
Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu Ser
70 75 80

gac tca cac ctg gca ccc tgg cag ctc aga gct ttt gtg tgt cgt ttt 464
Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg Phe
85 90 95

tct tcg gtg ata ttt tat gag acc atg tat gtg ggc atc gtg ctg tta 512
Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu Leu
100 105 110

ggg ctc ata gcc ttt gac aga ttc ctc aag atc atc aga cct ttg aga 560
Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu Arg
115 120 125

aat att ttt cta aaa aaa cct gtt ttt gca aaa acg gtc tca atc ttc 608
Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile Phe
130 135 140 145

atc tgg ttc ttt ttg ttc atc tcc ctg cca aat acg atc ttg agc 656
Ile Trp Phe Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu Ser
150 155 160

aac aag gaa gca aca cca tcg tct gtg aaa aag tgt gct tcc tta aag 704
Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu Lys
165 170 175

ggg cct ctg ggg ctg aaa tgg cat caa atg gta aat aac ata tgc cag 752
Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys Gln
180 185 190

ttt att ttc tgg act gtt ttt atc cta atg ctt gtg ttt tat gtg gtt 800

Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val Val			
195	200	205	
att gca aaa aaa gta tat gat tct tat aga aag tcc aaa agt aag gac			848
Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys Asp			
210	215	220	225
aga aaa aac aac aaa aag ctg gaa ggc aaa gta ttt gtt gtc gtg gct			896
Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val Ala			
230	235	240	
gtc ttc ttt gtg ttt gct cca ttt cat ttt gcc aga gtt cca tat			944
Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro Tyr			
245	250	255	
act cac agtcaa acc aac aat aag act gac tgt aga ctg caa aat caa			992
Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn Gln			
260	265	270	
ctg ttt att gct aaa gaa aca act ctc ttt ttg gca gca act aac att			1040
Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn Ile			
275	280	285	
tgt atg gat ccc tta ata tac ata ttc tta tgt aaa aaa ttc aca gaa			1088
Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Phe Thr Glu			
290	295	300	305
aag cta cca tgt atg caa ggg aga aag acc aca gca tca agc caa gaa			1136
Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln Glu			
310	315	320	
aat cat agc agt cag aca gac aac ata acc tta ggc tga caactgtaca			1185
Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly			
325	330		
tagggtaac ttctatttat tgatgagact tccgtagata atgtggaaat caaatttaac			1245
caagaaaaaa agatttggaaac aaatgtctc ttacattta ttatcctcggt gtacagaaaa			1305
gattatataa aatttaaatc cacatagatc tattcataag ctgaatgaac cattactaag			1365
agaatgcaac aggataaaaa tggccactag aggtcattat ttctttcttt cttttttttt			1425
tttttaatt tcaagagcat ttcaacttaa cattttggaa aagactaagg agaaacgtat			1485
atccctacaa acctccccctc caaacacctt ctcacattct tttccacaat tcacataaca			1545
ctactgcttt tggcccccattt aatgttagat atgtgctgaa agaaaaaaa aacgccccac			1605
tcttgaagtc cattgctgaa aactgcagcc aggggttgaa agggatgcag acttgaagag			1665
tctgaggaac tgaagtgggt cagcaagacc tctgaaatcc tgggtaaagg attttcct			1725
tacaattaca aacagcctct ttcacattac aataatatac cataggaggc acaagcacca			1785
ttattaagcc actttgctta caccttaagt gtgtacaatt caagtgtgag aatgctgtgt			1845
taactattct ttgaaattct ccttctgtcc agcaaatact ctaatgatgg ttaaacatgg			1905
cacctactca gcaatgcctt cctggaccac aacccctatc cccctgcccc accctcctca			1965

ttaaaaacaa atacttctac tgtttgggtg tgtgataaggg ttctcaatgc agatctccct 2025
tttctagtta gctatattct tgactgcate cgctaaaaat gttaaagctt cttgagagac 2085
agacatgcca gattttcttg gtatctccca taatacgacc tacagtccat ggtctacaga 2145
tgttttaat agaattgcta ttctcgatac atacaaagac gtaattgctg acccacaatc 2205
agtaacatcc atattgagag attttcaaa ggatggtgac cctgcttgta tttatttacc 2265
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gatggataag agtctacatc ttctagaaaa aatacataaa ggagtagtta agctctgtaa 2385
atgtgccacg agtccaaaca cgaccatcgt agggtaaagc ccacgtttc ttccatgcc 2445
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caccacacat gtatatttcc ccctggtaca cttggaagac tcttatccat ctgtgaaacc 2625
ctatgttgc atcacttggt ccatgaaata ttacctggcc aatatcccac catcacctca 2685
aaccatca cccctccctc tgtatgctgt cacacctata ttatcaaact tatcacattg 2745
cattgttaatt acttcctgac ctgttatct actcttttag taactgatgt atatatctga 2805
aaggagagat tgtttcattg tgcaatcaat aaatgtttga taaaataaag ccc 2858

<210> 19
<211> 333
<212> PRT
<213> Homo sapiens

<400> 19

Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro
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Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val
20 25 30

Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe
35 40 45

Val His Ile Pro Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
50 55 60

Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
65 70 75 80

Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
85 90 95

Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
100 105 110

Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu
115 120 125

Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile
130 135 140

Phe Ile Trp Phe Phe Leu Phe Ile Ser Leu Pro Asn Thr Ile Leu
145 150 155 160

Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu
165 170 175

Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
180 185 190

Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val
195 200 205

Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys
210 215 220

Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val
225 230 235 240

Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro
245 250 255

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
275 280 285

Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr
290 295 300

Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
305 310 315 320

Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly
325 330

<210> 20
<211> 878
<212> DNA
<213> Homo sapiens

<400> 20
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aataattatt tttaaaagtc acaaatacaa tcgtggata aagtcatgg ggcataaagt 120
atctcttaaa tatgtggcaa actatttgc caaagagatg tggtccaaac ccgtcgaagg 180
ctttataatt tggtatttata taacaagggtg aacaaaactg acaataaata ctccaaacgaa 240
ttatTTTTTaaataactaag gggcaaaggc tattctaagg ggcaaaacaa tctattactc 300
agacctaccc gaaaatttca cgtgaagtcg atcaaaagtt atacaaaatt ggtatTTTaca 360
tggTTTTaaat ccggattggc attttcttt aataataata catacaaaaa ctcagagggt 420
taataaagaa ataattcaaa gtcctaataa gtcaacaaac agatttcatt ataagctgga 480
acataaaaaga gacaccatgg ttggctgtct ctTTTcaaaa attatcacgg ccacttggc 540
aaacgggaag cagcatttag aacaatggtt ctcaaatctc ggggtggcat aaacaccatg 600
caggttggtt accacacaga ttccctggcc tggcccagt ctgaagctct cataaaggat 660
ctgaggaatc tgcttcgtga caagatttag actatttatt tatttacac ccaagctgga 720
gtgcagggggt gcaacccggc cagggaaacct cgcctcggag taaaaggaa accaaatcgg 780
ggcccaggcc ctgagaatgg gttcaaacgg gcccaccacc ggtaacggta tcagaaaaaa 840
acggtccaga aggccagggg tcaaccgaac caagaagc 878

<210> 21
<211> 1646
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (99)..(743)

<400> 21
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tgccaaagcc tgaaggctcc aagccataaa caacccca atg gcc tcc cac gaa gtt 116
Met Ala Ser His Glu Val
1 5
gat aat gca gag ctg ggg tca gcc tct gcc cat ggt acc cca ggc agt 164
Asp Asn Ala Glu Leu Gly Ser Ala Ser Ala His Gly Thr Pro Gly Ser
10 15 20
gag acg gga cca gaa gag ctg aat act tct gtc tac cac ccc ata aat 212
Glu Thr Gly Pro Glu Glu Leu Asn Thr Ser Val Tyr His Pro Ile Asn
25 30 35

gga tca cca gat tat cag aaa gca aaa tta caa gtt ctt ggg gcc atc Gly Ser Pro Asp Tyr Gln Lys Ala Lys Leu Gln Val Leu Gly Ala Ile 40 45 50	260
cag atc ctg aat gca gca atg att ctg gct ttg ggt gtc ttt ctg ggt Gln Ile Leu Asn Ala Ala Met Ile Leu Ala Leu Gly Val Phe Leu Gly 55 60 65 70	308
tcc ttg caa tac cca tac cac ttc caa aag cac ttc ttt ttc ttc acc Ser Leu Gln Tyr Pro Tyr His Phe Gln Lys His Phe Phe Phe Thr 75 80 85	356
ttc tac aca ggc tac ccg att tgg ggt gct gtg ttt ttc tgt agt tca Phe Tyr Thr Gly Tyr Pro Ile Trp Gly Ala Val Phe Phe Cys Ser Ser 90 95 100	404
gga acc ttg tct gtt gta gca ggg ata aaa ccc aca aga aca tgg ata Gly Thr Leu Ser Val Val Ala Gly Ile Lys Pro Thr Arg Thr Trp Ile 105 110 115	452
cag aac agt ttt gga atg aac att gcc agt gct aca att gca cta gtg Gln Asn Ser Phe Gly Met Asn Ile Ala Ser Ala Thr Ile Ala Leu Val 120 125 130	500
ggg act gct ttt ctc tca cta aat ata gca gtt aat atc cag tca tta Gly Thr Ala Phe Leu Ser Leu Asn Ile Ala Val Asn Ile Gln Ser Leu 135 140 145 150	548
agg agt tgt cac tct tca tca gag tca ccg gac cta tgc aat tac atg Arg Ser Cys His Ser Ser Glu Ser Pro Asp Leu Cys Asn Tyr Met 155 160 165	596
ggc tcc ata tca aat ggc atg gtg tct cta ctg ctg att ctc acc ttg Gly Ser Ile Ser Asn Gly Met Val Ser Leu Leu Leu Ile Leu Thr Leu 170 175 180	644
ctg gaa tta tgc gta act atc tct acc ata gcc atg tgg tgc aat gca Leu Glu Leu Cys Val Thr Ile Ser Thr Ile Ala Met Trp Cys Asn Ala 185 190 195	692
aac tgc tgt aat tca aga gag gaa att tcc tca cct ccc aat tct gtg Asn Cys Cys Asn Ser Arg Glu Glu Ile Ser Ser Pro Pro Asn Ser Val 200 205 210	740
taa tcaagaatac ctccttatga aaataattct gagagcatga atatttgacc	793
ttaaatctcc agtgactcag agcttcaccc acaaactcag gagaacataa gcctgctcgt	853
aaagctcaat ccttctatca tggcaccaat cacaagaacc ttggacgttt gactgactct	913
atcctttctc tcctaactat aaatcctatt tgggtgtcgt gggatggaa ggacagatat	973
atttctttag gcattcttgg atatctgtaa cttctatgtat cattactcca aagttgttc	1033
cagaaattgg ttctatccat tcttatccac ctactccatt gctttatgag gtttaaggaa	1093
ggaaggcggt ataatcccta ttcaatataat ttttctaaa atccaaacttc tgaccgccc	1153
gttagaagaa aaatgagaca tttttccat tacagagaaa tgcttcttga cttaacatc	1213

agcattataa aaagtgtcaa ataaaaaatt accatcatta tcattaaaat aaattttcac	1273
tgtatttgag atgggagggt taaggctcag ggattttatt tcagtgaact gctggaactc	1333
acacatgccc tgatatgtaa atgatgattt atgttggcga gtctgagagc aagccaaat	1393
gtgttcttca aaggacaatg ggaaactgta aagtagagaa ctaaagaata aggcccttag	1453
aatctgacac atctgggttc aaattctgaa actgtcactt attacctgta tgaacatggg	1513
caaattatct aatctctctg atctatttt cctcatctgt aaaataggtg taataataac	1573
aactacttg tcggttgctc tgagggttaa atgaaaataa aaagaaaatg tgaaacagca	1633
ccacaggtac ttg	1646

<210> 22
<211> 214
<212> PRT
<213> Homo sapiens

<400> 22

Met Ala Ser His Glu Val Asp Asn Ala Glu Leu Gly Ser Ala Ser Ala
1 5 10 15

His Gly Thr Pro Gly Ser Glu Thr Gly Pro Glu Glu Leu Asn Thr Ser
20 25 30

Val Tyr His Pro Ile Asn Gly Ser Pro Asp Tyr Gln Lys Ala Lys Leu
35 40 45

Gln Val Leu Gly Ala Ile Gln Ile Leu Asn Ala Ala Met Ile Leu Ala
50 55 60

Leu Gly Val Phe Leu Gly Ser Leu Gln Tyr Pro Tyr His Phe Gln Lys
65 70 75 80

His Phe Phe Phe Thr Phe Tyr Thr Gly Tyr Pro Ile Trp Gly Ala
85 90 95

Val Phe Phe Cys Ser Ser Gly Thr Leu Ser Val Val Ala Gly Ile Lys
100 105 110

Pro Thr Arg Thr Trp Ile Gln Asn Ser Phe Gly Met Asn Ile Ala Ser
115 120 125

Ala Thr Ile Ala Leu Val Gly Thr Ala Phe Leu Ser Leu Asn Ile Ala
130 135 140

Val Asn Ile Gln Ser Leu Arg Ser Cys His Ser Ser Glu Ser Pro

145

150

155

160

Asp Leu Cys Asn Tyr Met Gly Ser Ile Ser Asn Gly Met Val Ser Leu
165 170 175

Leu Leu Ile Leu Thr Leu Leu Glu Leu Cys Val Thr Ile Ser Thr Ile
180 185 190

Ala Met Trp Cys Asn Ala Asn Cys Cys Asn Ser Arg Glu Glu Ile Ser
195 200 205

Ser Pro Pro Asn Ser Val
210

<210> 23

<211> 2481

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (179)..(1276)

<400> 23

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ggttgcaagg cagttctgct ccccatcgtc ctcttgctga ctggggactg ctgagcccg 120

gcacggcaga gagtctggtg gggtgaggg gctggcctgg cccctctgtc ctgtggaa 178

atg ctg ggg caa gtg gtc acc ctc ata ctc ctc ctg ctc aag gtg 226
Met Leu Gly Gln Val Val Thr Leu Ile Leu Leu Leu Lys Val
1 5 10 15

tat cag ggc aaa gga tgc cag gga tca gct gac cat gtg gtt agc atc 274
Tyr Gln Gly Lys Gly Cys Gln Gly Ser Ala Asp His Val Val Ser Ile
20 25 30

tcg gga gtg cct ctt cag tta caa cca aac agc ata cag acg aag gtt 322
Ser Gly Val Pro Leu Gln Leu Gln Pro Asn Ser Ile Gln Thr Lys Val
35 40 45

gac agc att gca tgg aag aag ttg ctg ccc tca caa aat gga ttt cat 370
Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His
50 55 60

cac ata ttg aag tgg gag aat ggc tct ttg cct tcc aat act tcc aat 418
His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn
65 70 75 80

gat aga ttc agt ttt ata gtc aag aac ttg agt ctt ctc atc aag gca 466
Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala
85 90 95

gct cag cag cag gac agt ggc ctc tac tgc ctg gag gtc acc agt ata 514

Ala Gln Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile		
100	105	110
tct gga aaa gtt cag aca gcc acg ttc cag gtt ttt gta ttt gat aaa		562
Ser Gly Lys Val Gln Thr Ala Thr Phe Gln Val Phe Val Phe Asp Lys		
115	120	125
gtt gag aaa ccc cgc cta cag ggg cag ggg aag atc ctg gac aga ggg		610
Val Glu Lys Pro Arg Leu Gln Gly Gln Gly Lys Ile Leu Asp Arg Gly		
130	135	140
aga tgc caa gtg gct ctg tct tgc ttg gtc tcc agg gat ggc aat gtg		658
Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val		
145	150	155
160		
tcc tat gct tgg tac aga ggg agc aag ctg atc cag aca gca ggg aac		706
Ser Tyr Ala Trp Tyr Arg Gly Ser Lys Leu Ile Gln Thr Ala Gly Asn		
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ctc acc tac ctg gac gag gag gtt gac att aat ggc act cac aca tat		754
Leu Thr Tyr Leu Asp Glu Glu Val Asp Ile Asn Gly Thr His Thr Tyr		
180	185	190
acc tgc aat gtc agc aat cct gtt agc tgg gaa agc cac acc ctg aat		802
Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn		
195	200	205
ctc act cag gac tgt cag aat gcc cat cag gaa ttc aga ttt tgg ccg		850
Leu Thr Gln Asp Cys Gln Asn Ala His Gln Glu Phe Arg Phe Trp Pro		
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ttt ttg gtg atc atc gtg att cta agc gca ctg ttc ctt ggc acc ctt		898
Phe Leu Val Ile Ile Val Ile Leu Ser Ala Leu Phe Leu Gly Thr Leu		
225	230	235
240		
gcc tgc ttc tgt gtg tgg agg aga aag agg aag gag aag cag tca gag		946
Ala Cys Phe Cys Val Trp Arg Arg Lys Arg Lys Glu Lys Gln Ser Glu		
245	250	255
acc agt ccc aag gaa ttt ttg aca att tac gaa gat gtc aag gat ctg		994
Thr Ser Pro Lys Glu Phe Leu Thr Ile Tyr Glu Asp Val Lys Asp Leu		
260	265	270
aaa acc agg aga aat cac gag cag gag cag act ttt cct gga ggg ggg		1042
Lys Thr Arg Arg Asn His Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly		
275	280	285
agc acc atc tac tct atg atc cag tcc cag tct tct gct ccc acg tca		1090
Ser Thr Ile Tyr Ser Met Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser		
290	295	300
caa gaa cct gca tat aca tta tat tca tta att cag cct tcc agg aag		1138
Gln Glu Pro Ala Tyr Thr Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys		
305	310	315
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tct gga tcc agg aag agg aac cac agc cct tcc ttc aat agc act atc		1186
Ser Gly Ser Arg Lys Arg Asn His Ser Pro Ser Phe Asn Ser Thr Ile		
325	330	335
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Tyr Glu Val Ile Gly Lys Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg		

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Tyr Gln Gly Lys Gly Cys Gln Gly Ser Ala Asp His Val Val Ser Ile

20

25

30

Ser Gly Val Pro Leu Gln Leu Gln Pro Asn Ser Ile Gln Thr Lys Val
35 40 45

Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His
50 55 60

His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn
65 70 75 80

Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala
85 90 95

Ala Gln Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile
100 105 110

Ser Gly Lys Val Gln Thr Ala Thr Phe Gln Val Phe Val Phe Asp Lys
115 120 125

Val Glu Lys Pro Arg Leu Gln Gly Gln Gly Lys Ile Leu Asp Arg Gly
130 135 140

Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val
145 150 155 160

Ser Tyr Ala Trp Tyr Arg Gly Ser Lys Leu Ile Gln Thr Ala Gly Asn
165 170 175

Leu Thr Tyr Leu Asp Glu Glu Val Asp Ile Asn Gly Thr His Thr Tyr
180 185 190

Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn
195 200 205

Leu Thr Gln Asp Cys Gln Asn Ala His Gln Glu Phe Arg Phe Trp Pro
210 215 220

Phe Leu Val Ile Ile Val Ile Leu Ser Ala Leu Phe Leu Gly Thr Leu
225 230 235 240

Ala Cys Phe Cys Val Trp Arg Arg Lys Arg Lys Glu Lys Gln Ser Glu
245 250 255

Thr Ser Pro Lys Glu Phe Leu Thr Ile Tyr Glu Asp Val Lys Asp Leu
260 265 270

Lys Thr Arg Arg Asn His Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly
275 280 285

Ser Thr Ile Tyr Ser Met Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser
290 295 300

Gln Glu Pro Ala Tyr Thr Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys
305 310 315 320

Ser Gly Ser Arg Lys Arg Asn His Ser Pro Ser Phe Asn Ser Thr Ile
325 330 335

Tyr Glu Val Ile Gly Lys Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg
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attaacgtcc acatggagat atgaaagagg accggggatt ggtaccgtaa cc atg gtc
Met Val
1
agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc acc atg gca acc ttg 646
Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala Thr Leu

5	10	15	
tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag gat acc aca tta gag Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu 20 25 30			694
cca gaa gag cca cca acc aaa tac caa atc tct caa cca gaa gtg tac Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr 35 40 45 50			742
gtg gct gcg cca ggg gag tcg cta gag gtg cgc tgc ctg ttg aaa gat Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp 55 60 65			790
gcc gcc gtg atc agt tgg act aag gat ggg gtg cac ttg ggg ccc aac Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn 70 75 80			838
aat agg aca gtg ctt att ggg gag tac ttg cag ata aag ggc gcc acg Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly Ala Thr 85 90 95			886
cct aga gac tcc ggc ctc tat gct tgt act gcc agt agg act gta gac Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr Val Asp 100 105 110			934
agt gaa act tgg tac ttc atg gtg aat gtc aca gat gcc atc tca tcc Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser 115 120 125 130			982
gga gat gat gag gat gac acc gat ggt gcg gaa gat ttt gtc agt gag Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu 135 140 145			1030
aac agt aac aac aag aga gca cca tac tgg acc aac aca gaa aag atg Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met 150 155 160			1078
gaa aag cgg ctc cat gct gtg cct gcg gcc aac act gtc aag ttt cgc Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg 165 170 175			1126
tgc cca gcc ggg ggg aac cca atg cca acc atg cgg tgg ctg aaa aac Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn 180 185 190			1174
ggg aag gag ttt aag cag gag cat cgc att gga ggc tac aag gta cga Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg 195 200 205 210			1222
aac cag cac tgg agc ctc att atg gaa agt gtg gtc cca tct gac aag Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys 215 220 225			1270
gga aat tat acc tgt gtg gtg gag aat gaa tac ggg tcc atc aat cac Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His 230 235 240			1318
acg tac cac ctg gat gtt gtg gag cga tcg cct cac cgg ccc atc ctc Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu 245 250 255			1366

caa gcc gga ctg ccg gca aat gcc tcc aca gtg gtc gga gga gac gta Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val 260 265 270	1414
gag ttt gtc tgc aag gtt tac agt gat gcc cag ccc cac atc cag tgg Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp 275 280 285 290	1462
atc aag cac gtg gaa aag aac ggc agt aaa tac ggg ccc gac ggg ctg Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu 295 300 305	1510
ccc tac ctc aag gtt ctc aag cac tcg ggg ata aat agt tcc aat gca Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser Asn Ala 310 315 320	1558
gaa gtg ctg gct ctg ttc aat gtg acc gag gcg gat gct ggg gaa tat Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly Glu Tyr 325 330 335	1606
ata tgt aag gtc tcc aat tat ata ggg cag gcc aac cag tct gcc tgg Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser Ala Trp 340 345 350	1654
ctc act gtc ctg cca aaa cag caa gcg cct gga aga gaa aag gag att Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys Glu Ile 355 360 365 370	1702
aca gct tcc cca gac tac ctg gag ata gcc att tac tgc ata ggg gtc Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val 375 380 385	1750
ttc tta atc gcc tgt atg gtg gta aca gtc atc ctg tgc cga atg aag Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys 390 395 400	1798
aac acg acc aag aag cca gac ttc agc agc cag ccg gct gtg cac aag Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His Lys 405 410 415	1846
ctg acc aaa cgt atc ccc ctg cgg aga cag gta aca gtt tcg gct gag Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Glu 420 425 430	1894
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aca ctg ggc aag ccc ctg gga gaa ggt tgc ttt ggg caa gtg gtc atg Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met 485 490 495	2086

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gtg gcc gtg aag atg ttg aaa gat gat gcc aca gag aaa gac ctt tct Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser 515 520 525 530	2182
gat ctg gtg tca gag atg gag atg atg aag atg att ggg aaa cac aag Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys 535 540 545	2230
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ctg gcc aga ggc atg gag tac ttg gct tcc caa aaa tgt att cat cga Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg 615 620 625	2470
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aaa aag acc acc aat ggg cgg ctt cca gtc aag tgg atg gct cca gaa Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu 660 665 670	2614
gcc ctg ttt gat aga gta tac act cat cag agt gat gtc tgg tcc ttc Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe 675 680 685 690	2662
ggg gtg tta atg tgg gag atc ttc act tta ggg ggc tcg ccc tac cca Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro 695 700 705	2710
ggg att ccc gtg gag gaa ctt ttt aag ctg ctg aag gaa gga cac aga Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg 710 715 720	2758
atg gat aag cca gcc aac tgc acc aac gaa ctg tac atg atg atg agg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg 725 730 735	2806
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Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu			
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Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr			
755	760	765	770
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Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp			
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Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp			
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Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly			
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Ser Val Lys Thr			
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35 40 .45

Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
50 55 60

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65 70 75 80

Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
85 90 95

Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
100 105 110

Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
115 120 125

Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
130 135 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145 150 155 160

Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys

165

170

175

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
180 185 190

Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
195 200 205

Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
210 215 220

Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225 230 235 240

Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
245 250 255

Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
260 265 270

Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
275 280 285

Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
290 295 300

Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
305 310 315 320

Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
325 330 335

Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
340 345 350

Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
355 360 365

Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile
370 375 380

Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
385 390 395 400

Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val
405 410 415

His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
420 425 430

Ala Glu Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
435 440 445

Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val
450 455 460

Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
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Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
485 490 495

Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
500 505 510

Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
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Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
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His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro
545 550 555 560

Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
565 570 575

Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn
580 585 590

Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
595 600 605

Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
610 615 620

His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
625 630 635 640

Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
645 650 655

Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
660 665 670

Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
675 680 685

Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
690 695 700

Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
705 710 715 720

His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met
725 730 735

Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
740 745 750

Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Asn Glu
755 760 765

Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr
770 775 780

Pro Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser
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Met Gly Pro Trp Gly Trp Lys
1 5 114

ttg cgc tgg acc gtc gcc ttg ctc ctc gcc gcg ggg act gca gtg	162
Leu Arg Trp Thr Val Ala Leu Leu Ala Ala Ala Gly Thr Ala Val	
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ggc gac aga tgt gaa aga aac gag ttc cag tgc caa gac ggg aaa tgc	210
Gly Asp Arg Cys Glu Arg Asn Glu Phe Gln Cys Gln Asp Gly Lys Cys	
25 30 35	
atc tcc tac aag tgg gtc tgc gat ggc agc gct gag tgc cag gat ggc	258
Ile Ser Tyr Lys Trp Val Cys Asp Gly Ser Ala Glu Cys Gln Asp Gly	
40 45 50 55	
tct gat gag tcc cag gag acg tgc ttg tct gtc acc tgc aaa tcc ggg	306
Ser Asp Glu Ser Gln Glu Thr Cys Leu Ser Val Thr Cys Lys Ser Gly	
60 65 70	
gac ttc agc tgt ggg ggc cgt gtc aac cgc tgc att cct cag ttc tgg	354
Asp Phe Ser Cys Gly Gly Arg Val Asn Arg Cys Ile Pro Gln Phe Trp	
75 80 85	
agg tgc gat ggc caa gtg gac tgc gac aac ggc tca gac gag caa ggc	402
Arg Cys Asp Gly Gln Val Asp Cys Asp Asn Gly Ser Asp Glu Gln Gly	
90 95 100	
tgt ccc ccc aag acg tgc tcc cag gac gag ttt cgc tgc cac gat ggg	450
Cys Pro Pro Lys Thr Cys Ser Gln Asp Glu Phe Arg Cys His Asp Gly	
105 110 115	
aag tgc atc tct cgg cag ttc gtc tgt gac tca gac cgg gac tgc ttg	498
Lys Cys Ile Ser Arg Gln Phe Val Cys Asp Ser Asp Arg Asp Cys Leu	
120 125 130 135	
gac ggc tca gac gag gcc tcc tgc ccg gtg ctc acc tgt ggt ccc gcc	546
Asp Gly Ser Asp Glu Ala Ser Cys Pro Val Leu Thr Cys Gly Pro Ala	
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agc ttc cag tgc aac agc tcc acc tgc atc ccc cag ctg tgg gcc tgc	594
Ser Phe Gln Cys Asn Ser Ser Thr Cys Ile Pro Gln Leu Trp Ala Cys	
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gac aac gac ccc gac tgc gaa gat ggc tcg gat gag tgg ccg cag cgc	642
Asp Asn Asp Pro Asp Cys Glu Asp Gly Ser Asp Glu Trp Pro Gln Arg	
170 175 180	
tgt agg ggt ctt tac gtg ttc caa ggg gac agt agc ccc tgc tcg gcc	690
Cys Arg Gly Leu Tyr Val Phe Gln Gly Asp Ser Ser Pro Cys Ser Ala	
185 190 195	
ttc gag ttc cac tgc cta agt ggc gag tgc atc cac tcc agc tgg cgc	738
Phe Glu Phe His Cys Leu Ser Gly Glu Cys Ile His Ser Ser Trp Arg	
200 205 210 215	
tgt gat ggt ggc ccc gac tgc aag gac aaa tct gac gag gaa aac tgc	786
Cys Asp Gly Gly Pro Asp Cys Lys Asp Lys Ser Asp Glu Glu Asn Cys	
220 225 230	
gct gtg gcc acc tgt cgc cct gac gaa ttc cag tgc tct gat gga aac	834
Ala Val Ala Thr Cys Arg Pro Asp Glu Phe Gln Cys Ser Asp Gly Asn	
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gag gtc agg aag atg acg ctg gac cg ^g agc gag tac acc agc ctc atc Glu Val Arg Lys Met Thr Leu Asp Arg Ser Glu Tyr Thr Ser Leu Ile 410 415 420	1362
ccc aac ctg agg aac gtg gtc gct ctg gac acg gag gtg gcc agc aat Pro Asn Leu Arg Asn Val Val Ala Leu Asp Thr Glu Val Ala Ser Asn 425 430 435	1410
aga atc tac tgg tct gac ctg tcc cag aga atg atc tgc agc acc cag Arg Ile Tyr Trp Ser Asp Leu Ser Gln Arg Met Ile Cys Ser Thr Gln 440 445 450 455	1458
ctt gac aga gcc cac gg ^g gtc tct tcc tat gac acc gtc atc agc agg Leu Asp Arg Ala His Gly Val Ser Ser Tyr Asp Thr Val Ile Ser Arg 460 465 470	1506
gac atc cag gcc ccc gac ggg ctg gct gtg gac tgg atc cac agc aac Asp Ile Gln Ala Pro Asp Gly Leu Ala Val Asp Trp Ile His Ser Asn 475 480 485	1554
atc tac tgg acc gac tct gtc ctg ggc act gtc tct gtt gcg gat acc	1602

Ile Tyr Trp Thr Asp Ser Val Leu Gly Thr Val Ser Val Ala Asp Thr			
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Lys Gly Val Lys Arg Lys Thr Leu Phe Arg Glu Asn Gly Ser Lys Pro			
505	510	515	
agg gcc atc gtg gtg gat cct gtt cat ggc ttc atg tac tgg act gac			1698
Arg Ala Ile Val Val Asp Pro Val His Gly Phe Met Tyr Trp Thr Asp			
520	525	530	535
tgg gga act ccc gcc aag atc aag aaa ggg ggc ctg aat ggt gtg gac			1746
Trp Gly Thr Pro Ala Lys Ile Lys Gly Gly Leu Asn Gly Val Asp			
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Ile Tyr Ser Leu Val Thr Glu Asn Ile Gln Trp Pro Asn Gly Ile Thr			
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cta gat ctc ctc agt ggc cgc ctc tac tgg gtt gac tcc aaa ctt cac			1842
Leu Asp Leu Leu Ser Gly Arg Leu Tyr Trp Val Asp Ser Lys Leu His			
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tcc atc tca agc atc gat gtc aat ggg ggc aac cgg aag acc atc ttg			1890
Ser Ile Ser Ser Ile Asp Val Asn Gly Gly Asn Arg Lys Thr Ile Leu			
585	590	595	
gag gat gaa aag agg ctg gcc cac ccc ttc tcc ttg gcc gtc ttt gag			1938
Glu Asp Glu Lys Arg Leu Ala His Pro Phe Ser Leu Ala Val Phe Glu			
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gac aaa gta ttt tgg aca gat atc atc aac gaa gcc att ttc agt gcc			1986
Asp Lys Val Phe Trp Thr Asp Ile Ile Asn Glu Ala Ile Phe Ser Ala			
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aac cgc ctc aca ggt tcc gat gtc aac ttg ttg gct gaa aac cta ctg			2034
Asn Arg Leu Thr Gly Ser Asp Val Asn Leu Leu Ala Glu Asn Leu Leu			
635	640	645	
tcc cca gag gat atg gtc ctc ttc cac aac ctc acc cag cca aga gga			2082
Ser Pro Glu Asp Met Val Leu Phe His Asn Leu Thr Gln Pro Arg Gly			
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gtg aac tgg tgt gag agg acc acc ctg agc aat ggc ggc tgc cag tat			2130
Val Asn Trp Cys Glu Arg Thr Thr Leu Ser Asn Gly Gly Cys Gln Tyr			
665	670	675	
ctg tgc ctc cct gcc ccg cag atc aac ccc cac tcg ccc aag ttt acc			2178
Leu Cys Leu Pro Ala Pro Gln Ile Asn Pro His Ser Pro Lys Phe Thr			
680	685	690	695
tgc gcc tgc ccg gac ggc atg ctg ctg gcc agg gac atg agg agc tgc			2226
Cys Ala Cys Pro Asp Gly Met Leu Leu Ala Arg Asp Met Arg Ser Cys			
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ctc aca gag gct gag gct gca gtg gcc acc cag gag aca tcc acc gtc			2274
Leu Thr Glu Ala Glu Ala Ala Val Ala Thr Gln Glu Thr Ser Thr Val			
715	720	725	
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Arg Leu Lys Val Ser Ser Thr Ala Val Arg Thr Gln His Thr Thr Thr			

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Arg Pro Val Pro Asp Thr Ser Arg Leu Pro Gly Ala Thr Pro Gly Leu			
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acc acg gtg gag ata gtg aca atg tct cac caa gct ctg ggc gac gtt			2418
Thr Thr Val Glu Ile Val Thr Met Ser His Gln Ala Leu Gly Asp Val			
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gct ggc aga gga aat gag aag aag ccc agt agc gtg agg gct ctg tcc			2466
Ala Gly Arg Gly Asn Glu Lys Lys Pro Ser Ser Val Arg Ala Leu Ser			
780	785	790	
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Ile Val Leu Pro Ile Val Leu Leu Val Phe Leu Cys Leu Gly Val Phe			
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Leu Leu Trp Lys Asn Trp Arg Leu Lys Asn Ile Asn Ser Ile Asn Phe			
810	815	820	
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Asp Asn Pro Val Tyr Gln Lys Thr Thr Glu Asp Glu Val His Ile Cys			
825	830	835	
cac aac cag gac ggc tac agc tac ccc tcg aga cag atg gtc agt ctg			2658
His Asn Gln Asp Gly Tyr Ser Tyr Pro Ser Arg Gln Met Val Ser Leu			
840	845	850	855
gag gat gac gtg gcg tga acatctgcct ggagtccgc ccctgcccag			2706
Glu Asp Asp Val Ala			
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tactt	ggg	gg	gg	gg	gg	gg	gg	gg	4506
catgat	cgag	ccact	gc	cc	ct	gg	ca	ac	4566
aactata	aaa	aaa	aaa	aa	at	cc	cc	cc	4626
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agact	cccg	gt	ga	agat	gt	tt	cc	gg	4746
gtcccc	cc	gt	ca	gg	tt	cc	gg	gg	4806
ccct	gtac	at	gt	gg	tt	tt	tt	tt	4866
ttat	cact	ta	ta	ta	ta	ta	ta	ta	4926
tgg	tt	tt	tt	tt	tt	tt	tt	tt	4986
gaaat	gc	tc	t	c	t	t	t	t	5046
ttt	gg	gg	gg	gg	gg	gg	gg	gg	5106
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<212> PRT

<213> Homo sapiens

<400> 28

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35 40 45

Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln Glu Thr Cys Leu
50 55 60

Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly Gly Arg Val Asn
65 70 75 80

Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln Val Asp Cys Asp
85 90 95

Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp
100 105 110

Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys
115 120 125

Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro
130 135 140

Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn Ser Ser Thr Cys
145 150 155 160

Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp Cys Glu Asp Gly
165 170 175

Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr Val Phe Gln Gly
180 185 190

Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys Leu Ser Gly Glu
195 200 205

Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro Asp Cys Lys Asp
210 215 220

Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys Arg Pro Asp Glu

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Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser Arg Gln Cys Asp			
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Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val Gly Cys Val Asn			
260	265	270	
Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys His Ser Gly Glu			
275	280	285	
Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg Asp Cys Arg Asp			
290	295	300	
Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn Glu Cys Leu Asp			
305	310	315	320
Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu Lys Ile Gly Tyr			
325	330	335	
Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala Gln Arg Arg Cys			
340	345	350	
Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys Ser Gln Leu Cys			
355	360	365	
Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu Glu Gly Phe Gln			
370	375	380	
Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly Ser Ile Ala Tyr			
385	390	395	400
Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met Thr Leu Asp Arg			
405	410	415	
Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn Val Val Ala Leu			
420	425	430	
Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser Asp Leu Ser Gln			
435	440	445	
Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His Gly Val Ser Ser			
450	455	460	
Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro Asp Gly Leu Ala			
465	470	475	480

Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp Ser Val Leu Gly
485 490 495

Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg Lys Thr Leu Phe
500 505 510

Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val Asp Pro Val His
515 520 525

Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala Lys Ile Lys Lys
530 535 540

Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val Thr Glu Asn Ile
545 550 555 560

Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser Gly Arg Leu Tyr
565 570 575

Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile Asp Val Asn Gly
580 585 590

Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg Leu Ala His Pro
595 600 605

Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp Thr Asp Ile Ile
610 615 620

Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly Ser Asp Val Asn
625 630 635 640

Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met Val Leu Phe His
645 650 655

Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu Arg Thr Thr Leu
660 665 670

Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala Pro Gln Ile Asn
675 680 685

Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp Gly Met Leu Leu
690 695 700

Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu Ala Ala Val Ala
705 710 715 720

Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser Ser Thr Ala Val
725 730 735

Arg Thr Gln His Thr Thr Arg Pro Val Pro Asp Thr Ser Arg Leu
740 745 750

Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val Thr Met Ser
755 760 765

His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn Glu Lys Lys Pro
770 775 780

Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile Val Leu Leu Val
785 790 795 800

Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn Trp Arg Leu Lys
805 810 815

Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr Gln Lys Thr Thr
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Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly Tyr Ser Tyr Pro
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<211> 2070
<212> DNA
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ctc ccc aag ccc acc ctc tgg gct gag cca ggc tct gtg atc atc cag	Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val Ile Ile Gln	210
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45 50 55		
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60 65 70		
caa gag cct ggg aag aat ggc cag ttc ccc atc cca tcc atc acc tgg	Gln Glu Pro Gly Lys Asn Gly Gln Phe Pro Ile Pro Ser Ile Thr Trp	354
75 80 85		
gaa cac gca ggg cgg tat cac tgt cag tac tac agc cac aat cac tca	Glu His Ala Gly Arg Tyr His Cys Gln Tyr Ser His Asn His Ser	402
90 95 100 105		
tca gag tac agt gac ccc ctg gag ctg gtg aca gga gcc tac agc	Ser Glu Tyr Ser Asp Pro Leu Glu Leu Val Val Thr Gly Ala Tyr Ser	450
110 115 120		
aaa ccc acc ctc tca gct ctg ccc agc cct gtg gtg acc tta gga ggg	Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Val Val Thr Leu Gly Gly	498
125 130 135		
aac gtg acc ctc cag tgt gtc tca cag gtg gca ttt gac ggc ttc att	Asn Val Thr Leu Gln Cys Val Ser Gln Val Ala Phe Asp Gly Phe Ile	546
140 145 150		
ctg tgt aag gaa gga gaa gat gaa cac cca caa cgc ctg aac tcc cat	Leu Cys Lys Glu Gly Glu Asp Glu His Pro Gln Arg Leu Asn Ser His	594
155 160 165		
tcc cat gcc cgt ggg tgg tcc tgg gcc atc ttc tcc gtg ggc ccc gtg	Ser His Ala Arg Gly Trp Ser Trp Ala Ile Phe Ser Val Gly Pro Val	642
170 175 180 185		
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190 195 200		
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cgc cct ggt tgg cag ccc cag gct ggg ctc tcc cag gcc aac ttc acc Arg Pro Gly Trp Gln Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr 270 275 280	930
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ccg gtc ccc aca gta gcc cca gga aag aac gtg acc ctg ctg tgt cag Pro Val Pro Thr Val Ala Pro Gly Lys Asn Val Thr Leu Leu Cys Gln 330 335 340 345	1122
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agt gac ccc ctg gag ctc gtg gtc tca gca tcc cta ggc caa cac ccc Ser Asp Pro Leu Glu Leu Val Val Ser Ala Ser Leu Gly Gln His Pro 410 415 420 425	1362
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Arg Ser Leu Gln Asp Ala Ala Gly Arg
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<400> 31

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Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
20 25 30

Ala Glu Pro Gly Ser Val Ile Ile Gln Gly Ser Pro Val Thr Leu Arg
35 40 45

Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn
50 55 60

Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly
65 70 75 80

Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr His
85 90 95

Cys Gln Tyr Tyr Ser His Asn His Ser Ser Glu Tyr Ser Asp Pro Leu
100 105 110

Glu Leu Val Val Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu
115 120 125

Pro Ser Pro Val Val Thr Leu Gly Gly Asn Val Thr Leu Gln Cys Val
130 135 140

Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp
145 150 155 160

Glu His Pro Gln Arg Leu Asn Ser His Ser His Ala Arg Gly Trp Ser
165 170 175

Trp Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser
180 185 190

Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Val Trp Ser Leu
195 200 205

Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro
210 215 220

Ser Leu Ser Val Gln Pro Gly Pro Met Val Ala Pro Gly Glu Ser Leu
225 230 235 240

Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr
245 250 255

Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Trp Gln Pro Gln
260 265 270

Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Pro Ser
275 280 285

His Gly Gly Gln Tyr Arg Cys Tyr Ser Ala His Asn Leu Ser Ser Glu
290 295 300

Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Phe
305 310 315 320

Tyr Asp Arg Pro Ser Leu Ser Val Gln Pro Val Pro Thr Val Ala Pro
325 330 335

Gly Lys Asn Val Thr Leu Leu Cys Gln Ser Arg Gly Gln Phe His Thr
340 345 350

Phe Leu Leu Thr Lys Glu Gly Ala Gly His Pro Pro Leu His Leu Arg
355 360 365

Ser Glu His Gln Ala Gln Gln Asn Gln Ala Glu Phe Arg Met Gly Pro
370 375 380

Val Thr Ser Ala His Val Gly Thr Tyr Arg Cys Tyr Ser Ser Leu Ser
385 390 395 400

Ser Asn Pro Tyr Leu Leu Ser Leu Pro Ser Asp Pro Leu Glu Leu Val
405 410 415

Val Ser Ala Ser Leu Gly Gln His Pro Gln Asp Tyr Thr Val Glu Asn
420 425 430

Leu Ile Arg Met Gly Val Ala Gly Leu Val Leu Val Val Leu Gly Ile
435 440 445

Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Leu Gln Asp Ala Ala
450 455 460

Gly Arg
465